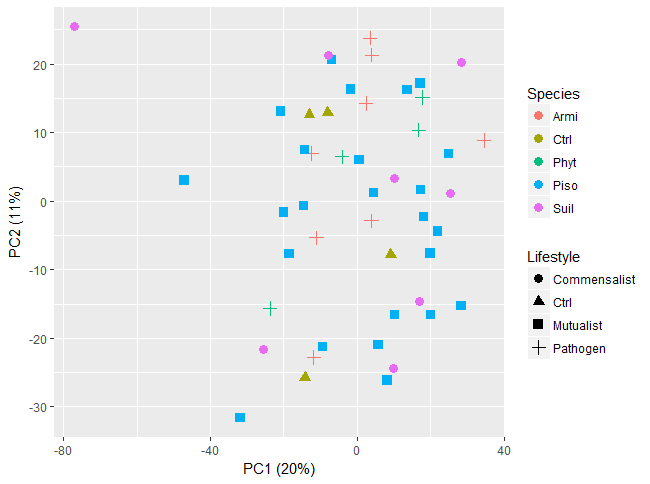
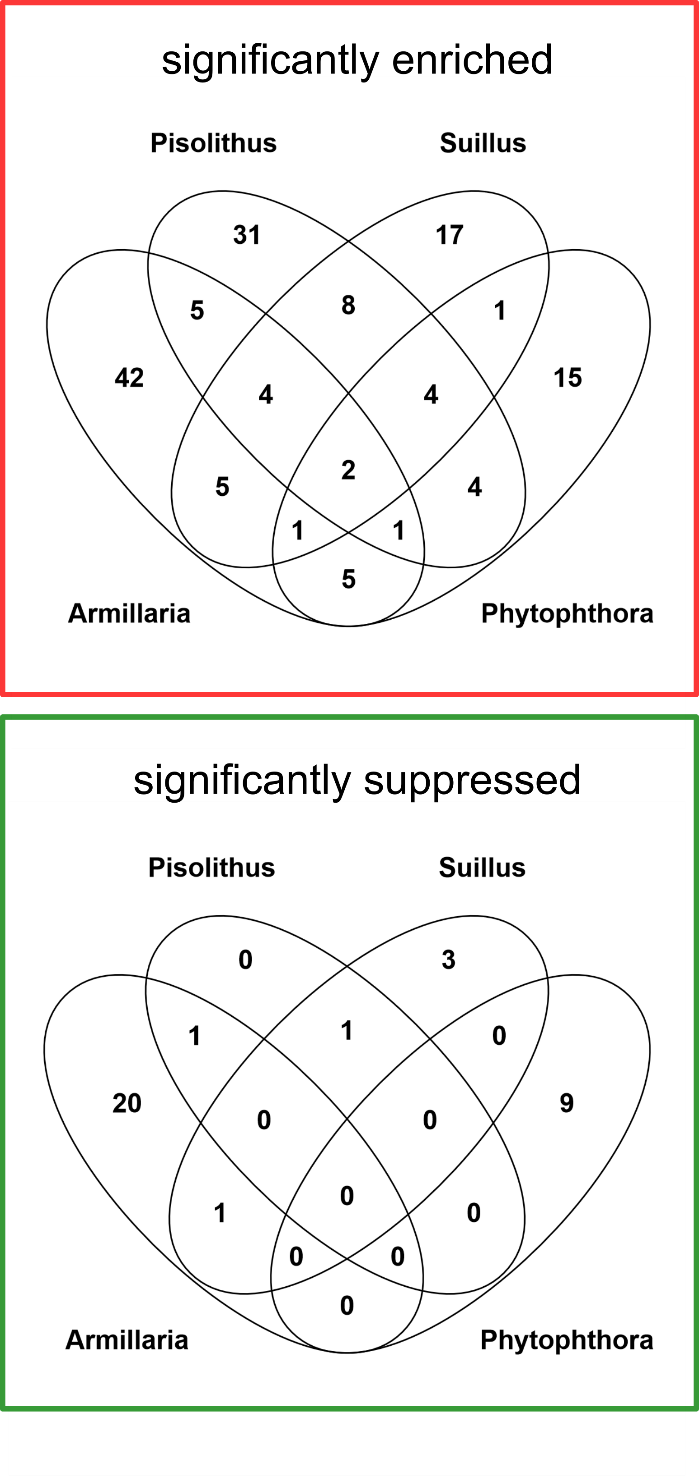
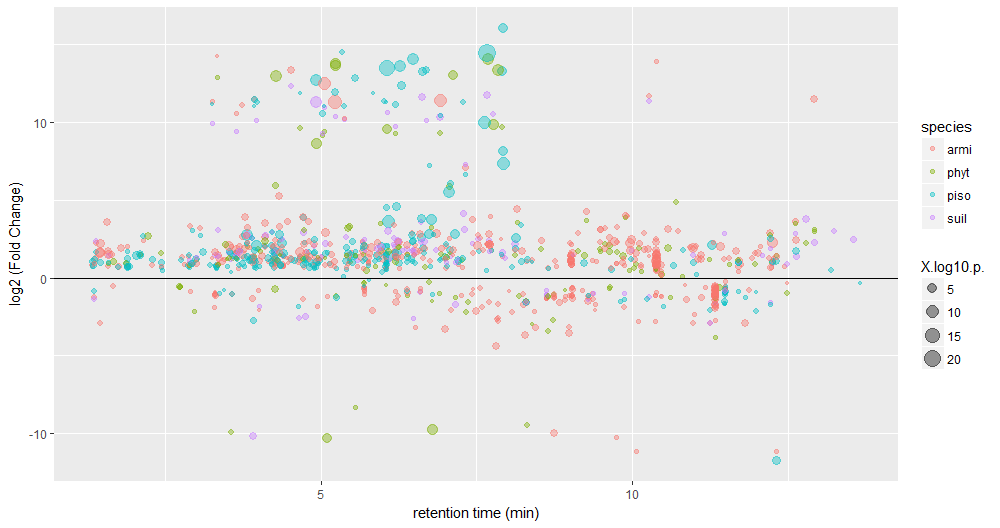
**Supplementary figures:**



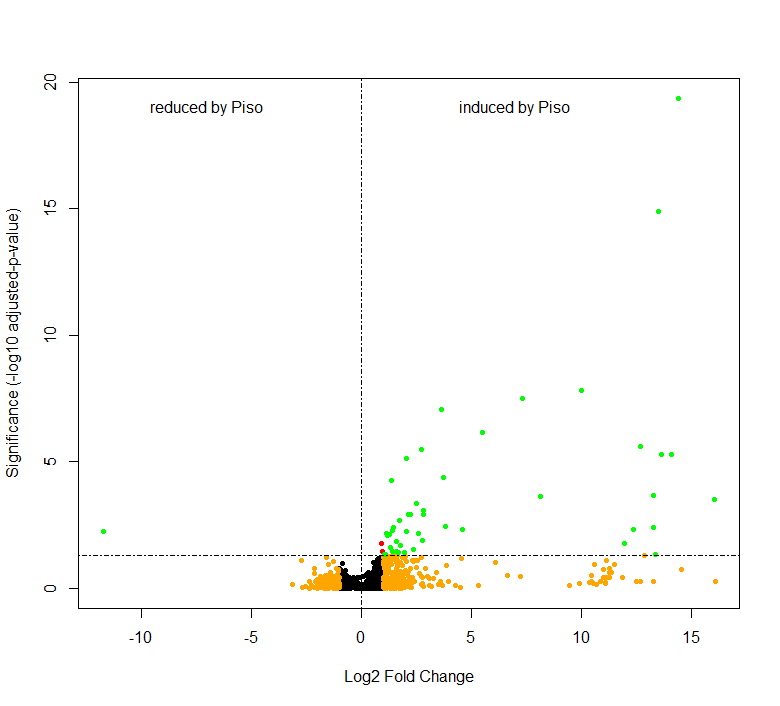
**Supplementary figure 1.** PCA score plot showing the variation among metabolite profiles (LC-MS ESI- mode) of *E. grandis* root tips after 24 h pre-symbiosis with different microbes. The color and shape of symbols represent the species and the lifestyles of the interacting microbes. armi = *Armillaria luteobubalina* ; piso = *Pisolithus microcarpus*; suil = *Suillus granulatus*; phyt = *Phytophthora cinnamomi*; ctrl = uninfected control

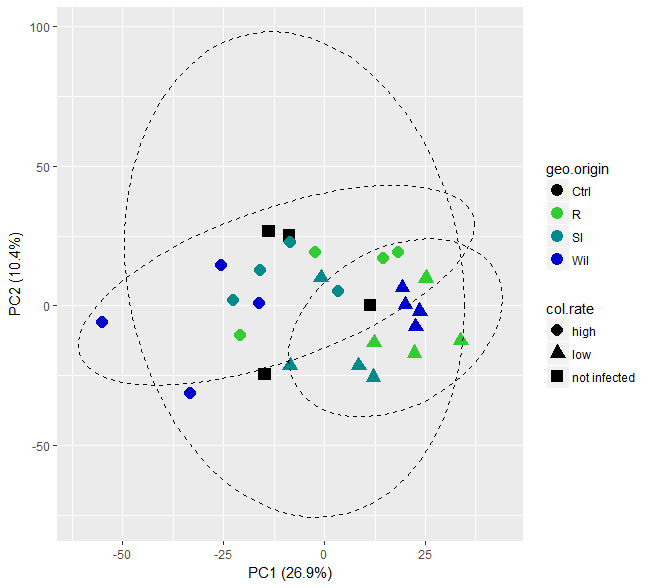


**Supplementary figure 2****.** Venn diagrams showing the significantly enriched and suppressed molecular features amongst different microbe-treated roots in comparison to the untreated control. Student t-test was performed for each pair of comparison between the control and the microbes-treated root tips. Significantly regulated molecular features profiled with ESI- mode that exhibit more than five-fold of intensity change and with *p* < 0.05 are shown in the Venn diagram.

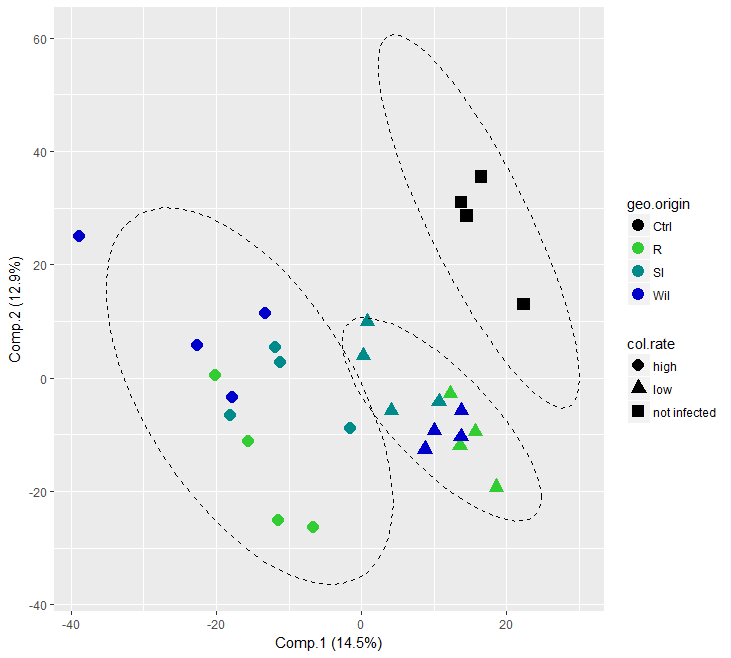


**Supplementary figure 3****.** The scatter plot showing distribution of the significantly regulated metabolites (*p* < 0.05) across the span of retention time of metabolite profiling in root tips after pre-symbiotic interaction with microbes of different species that are captured in LC-MS (ESI-).armi = *Armillaria luteobubalina* ; piso = *Pisolithus microcarpus*; suil = *Suillus granulatus*; phyt = *Phytophthora cinnamomi*

**Supplementary figure 4****.** Volcano plot showing the varied molecular features in *E. grandis* root tips after pre-symbiosis with *P. microcarpus* (n = 24) for 24 h in comparison to control root tips (n = 4). The metabolite profiles are derived from LC-MS (ESI- mode). The y-axis and x-axis correspond to the mean fold change of *Pisolithus*-interacting root tips in comparison to control, and the significance value in terms of *p*-value (adjusted by Bonferroni-method). Red = *p* < 0.05; Orange = Fold Change > 2; Green = *p* < 0.05 and Intensity fold change >2.



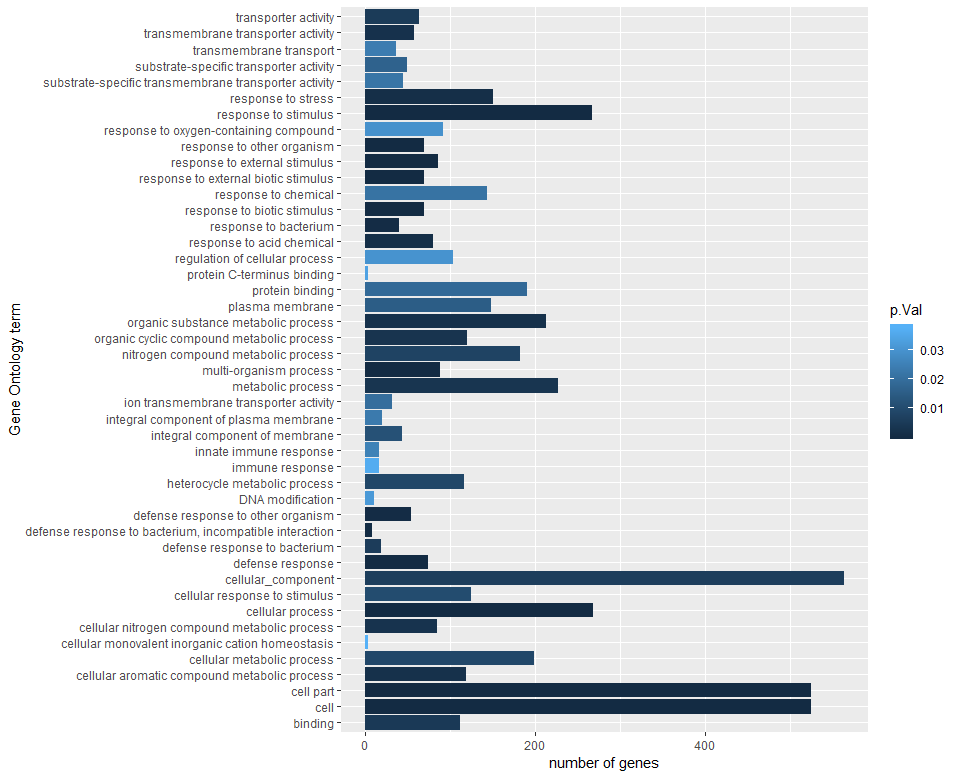
**Supplementary figure 5****.** PCA score plot showing the multivariate-variation among *Pisolithus*-interacting root tips samples in terms of metabolite profiles derived from the ESI- mode, LC-MS. The color of the symbols represents the geographical origin (geo. origin) of the *Pisolithus* strains, while the shape of the symbols represents the colonization rates (col. rate). Ctrl = un-infected control roots; R = Royal National Park; SI = Sussex Inlet; Wil = Wilberforce.



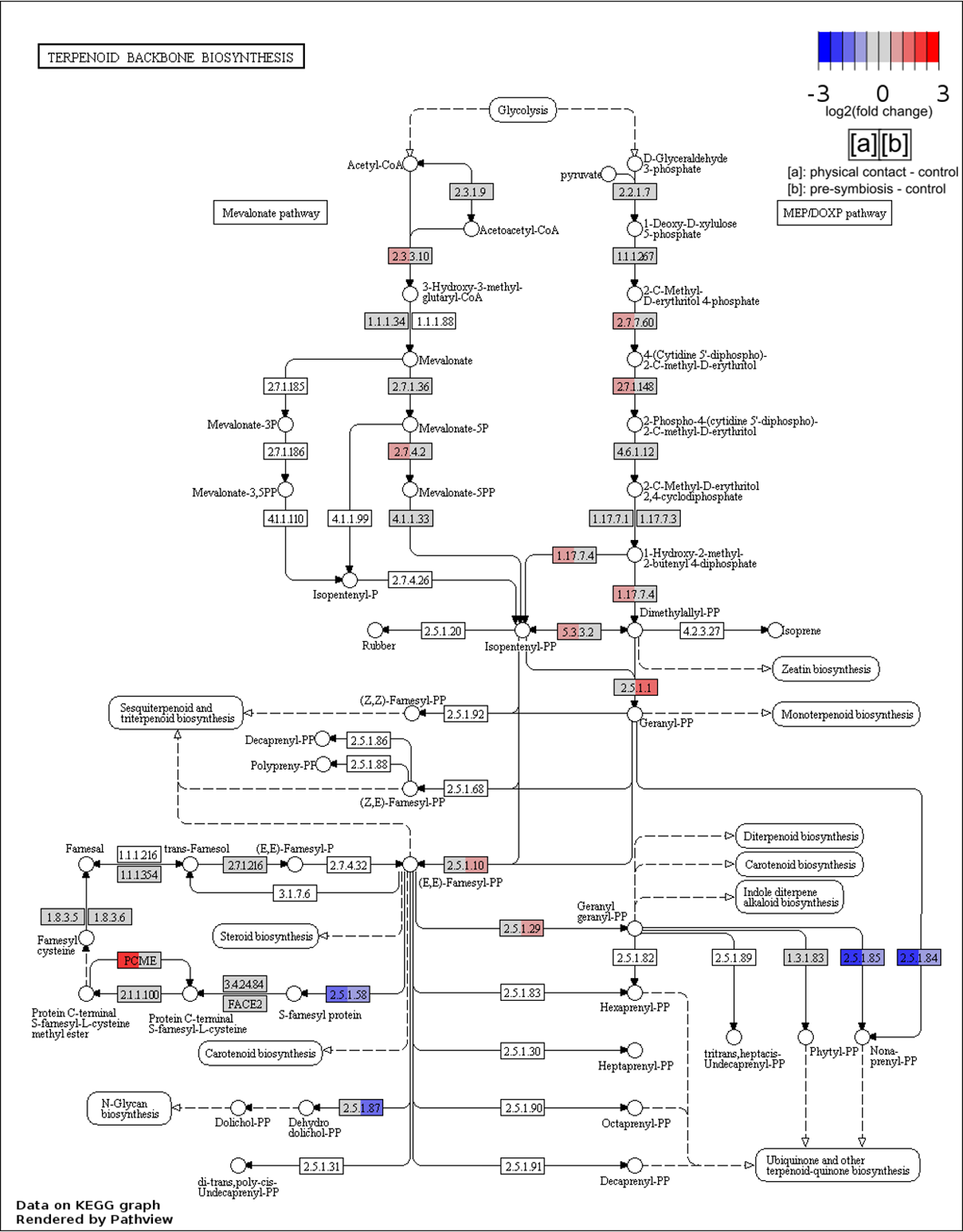
**Supplementary figure 6.** PLS-DA score plot showing the first two components of the supervised classification model that separates metabolite profiles of *Pisolithus*-interacting root tips samples (LC-MS ESI- mode) in terms of colonization rate. The color of the symbols represents the geographical origin (geo. origin) of the *Pisolithus* isolates, while the shape of the symbols represents the colonization rates (col. rate). Ctrl = un-infected control roots; R = Royal National Park; SI = Sussex Inlet; Wil = Wilberforce.



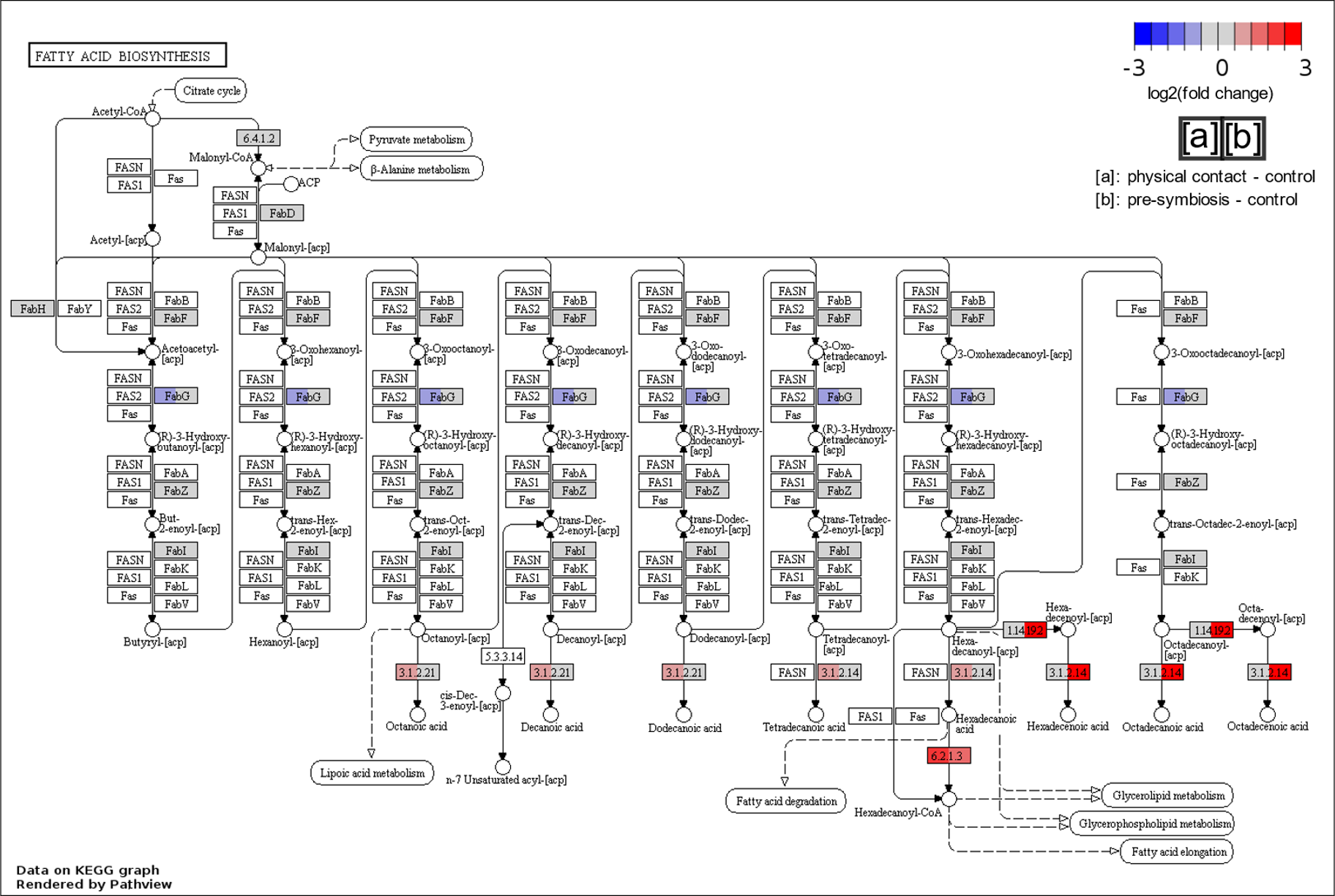
**Supplementary figure 7.** (Left) Scatter plot showing the abundance of 13C-labeled compounds in *Pisolithus*-treated root tips in labeled setup in relation to unlabeled setup, across the retention time span of LC-MS ESI- mode metabolite profiling. The color of the points showing the absolute intensity of the compound peak detected by the LC-MS. An unlabeled or mis-detected labelled metabolite would have a log (relative abundance) ≤ 0. (right) The violin plot demonstrates the distribution of 13C-labeled compounds with different relative abundance.

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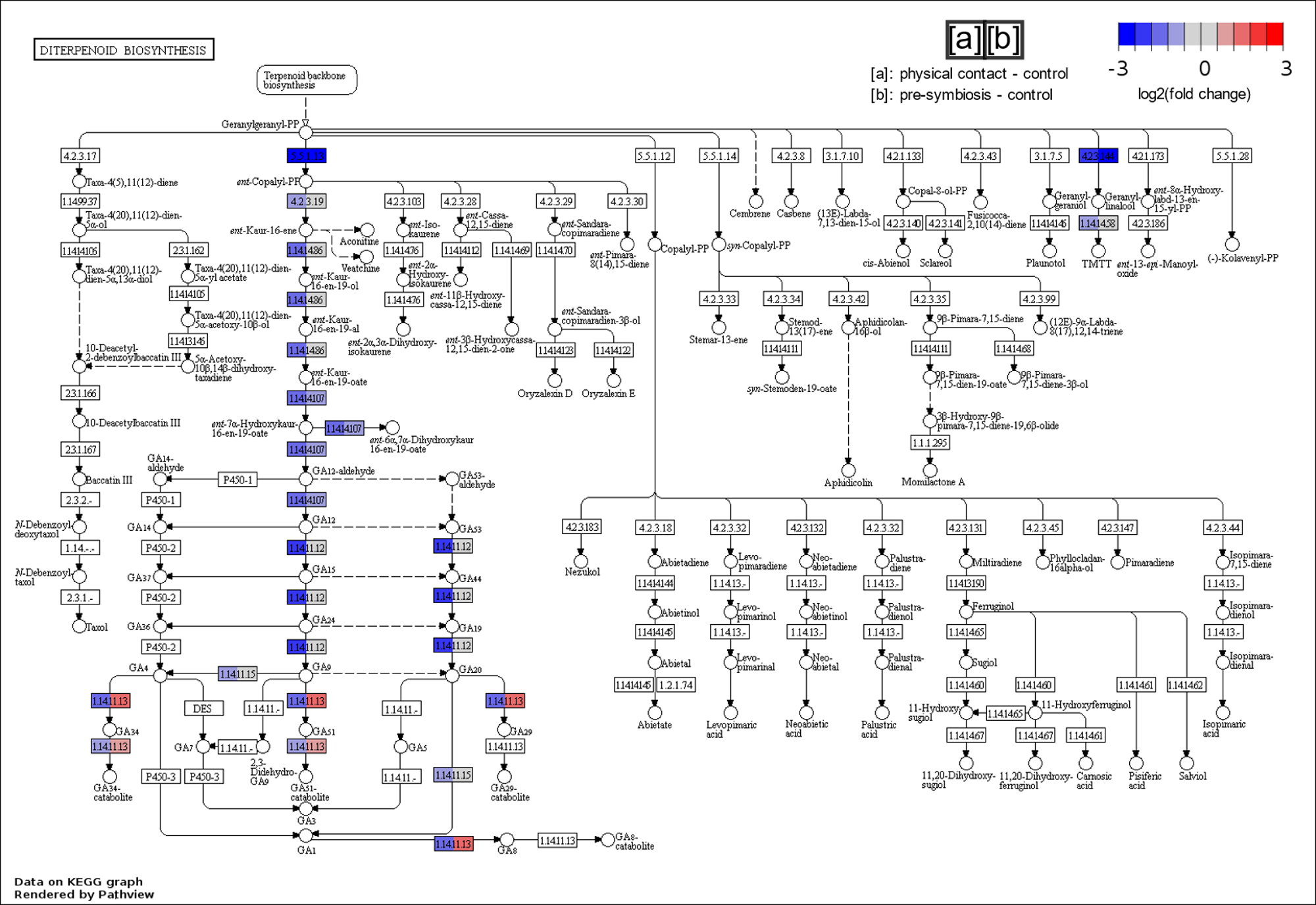
**Supplementary figure 8.** Gene ontology enrichment results for highly-induced genes (log2(fold change) >5) in *E. grandis* roots in the pre-symbiotic interaction. Bar plot represent the number of genes involved in a gene-set of the enriched gene ontology term. The darkness of the color of the bar represent the significance (in terms of p-values) of the enriched gene-sets.



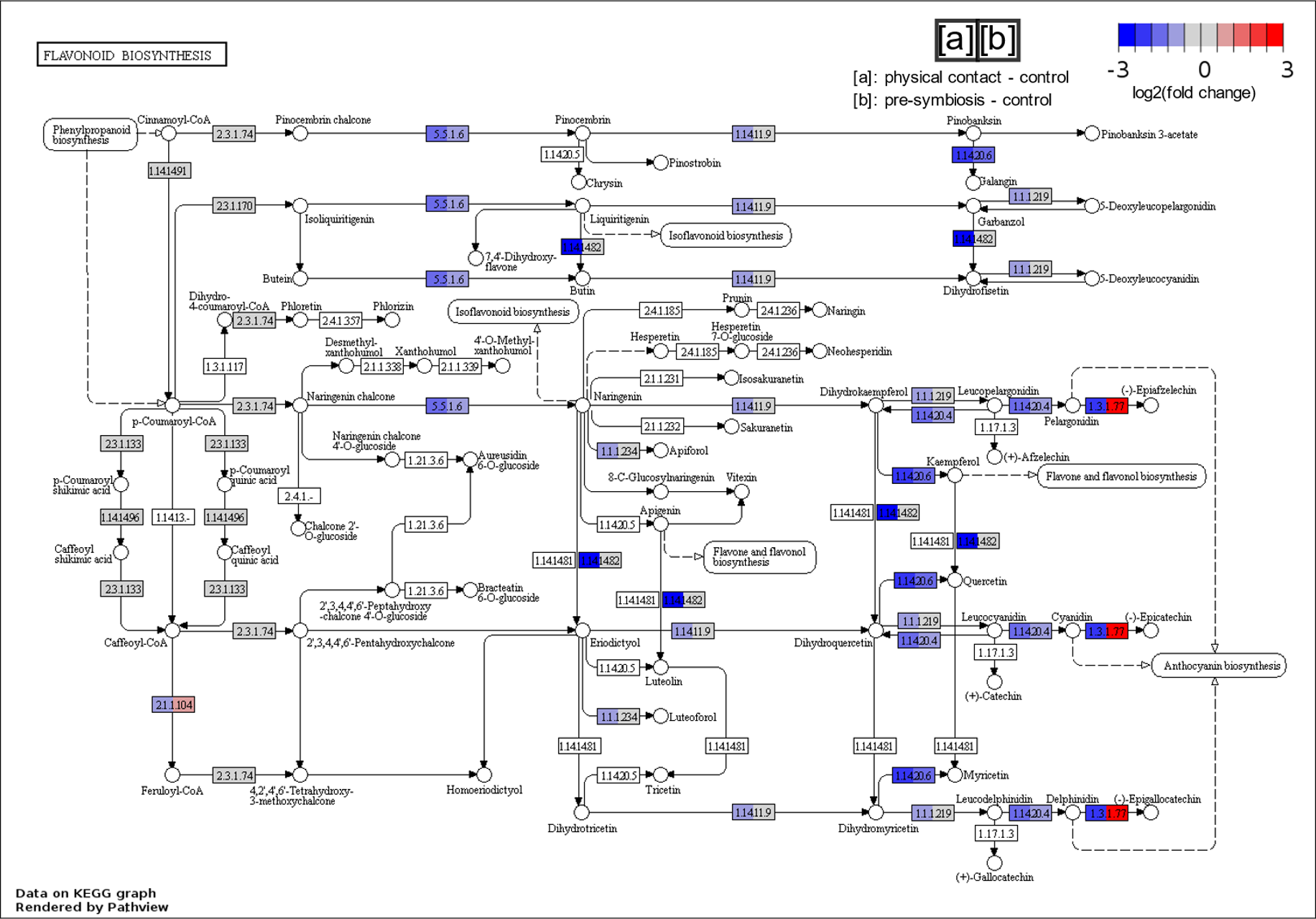
**Supplementary figure 9.** Pathway graph to visualize the genes associated with the terpenoid backbone biosynthesis pathway and their expressions in *E. grandis* roots during direct physical interaction (coloration on left-hand side of each enzyme box) and pre-symbiotic interaction (coloration on the right-hand side of each enzyme box) with *Pisolithus microcarpus* in comparison to uninfected control roots. The *Arabidopsis thaliana* homologs of the *E. grandis* genes and their expression were mapped onto the pathway. The color of the boxes represents the log2(fold change) value of the gene.



**Supplementary figure 10.** Pathway graph to visualize the genes associated with the fatty acid biosynthesis pathway and their expressions in *E. grandis* roots during direct physical interaction (coloration on left-hand side of each enzyme box) and pre-symbiotic interaction (coloration on the right-hand side of each enzyme box) with *Pisolithus microcarpus* in comparison to uninfected control roots. The *Arabidopsis thaliana* homologs of the *E. grandis* genes and their expression were mapped onto the pathway. The color of the boxes represents the log2(fold change) value of the gene.

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**Supplementary figure 11.** Pathway graph to visualize the genes associated with the diterpenoid biosynthesis pathway and their expressions in *E. grandis* roots during direct physical interaction (coloration on left-hand side of each enzyme box) and pre-symbiotic interaction (coloration on the right-hand side of each enzyme box) with *Pisolithus microcarpus* in comparison to uninfected control roots. The *Arabidopsis thaliana* homologs of the *E. grandis* genes and their expression were mapped onto the pathway. The color of the boxes represents the log2(fold change) value of the gene.

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**Supplementary figure 12.** Pathway graph to visualize the genes associated with the flavonoid biosynthesis pathway and their expressions in *E. grandis* roots during direct physical interaction (coloration on left-hand side of each enzyme box) and pre-symbiotic interaction (coloration on the right-hand side of each enzyme box) with *Pisolithus microcarpus* in comparison to uninfected control roots. The *Arabidopsis thaliana* homologs of the *E. grandis* genes and their expression were mapped onto the pathway. The color of the boxes represents the log2(fold change) value of the gene.